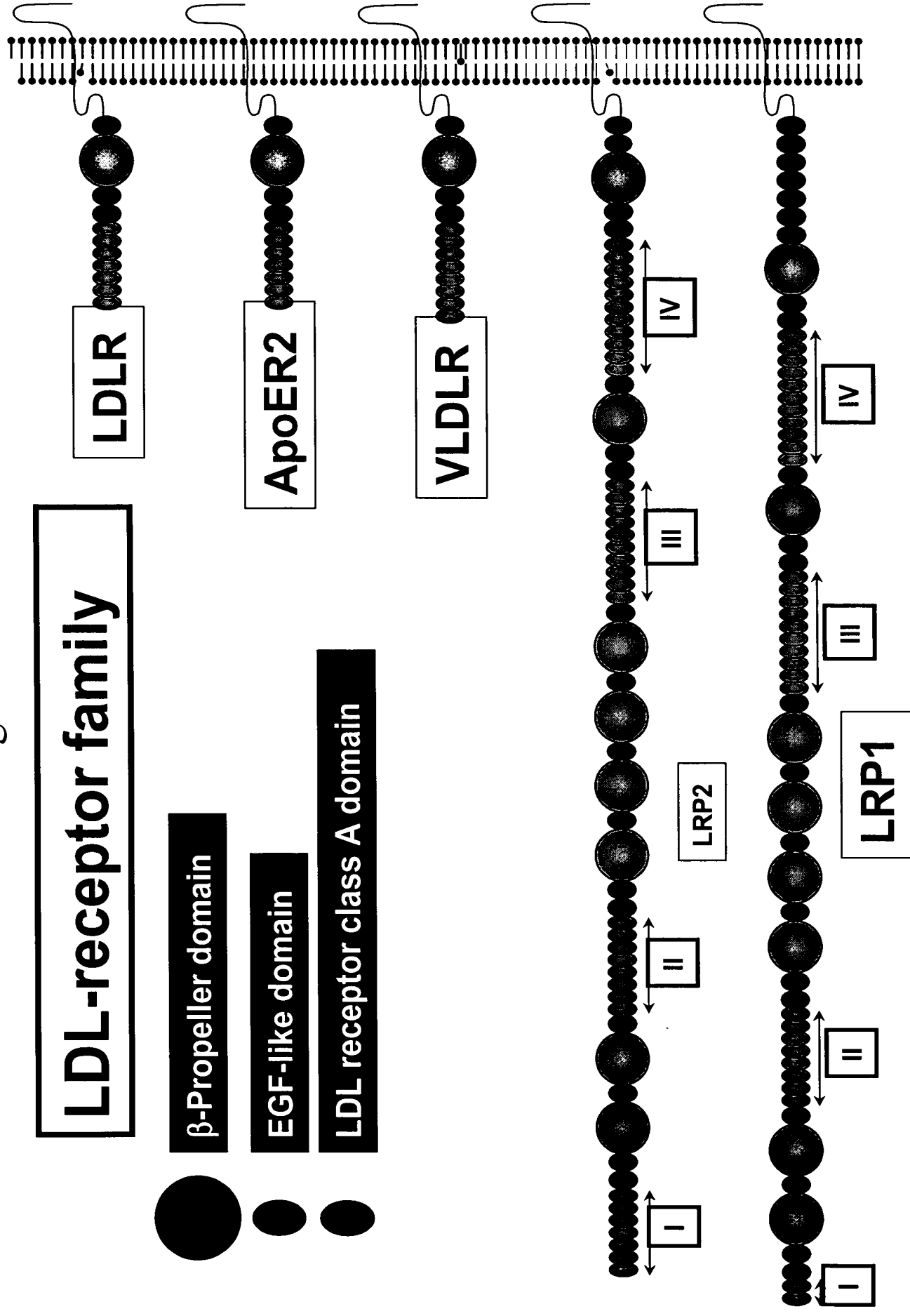


Figure 1



## LDL-receptor class A domain

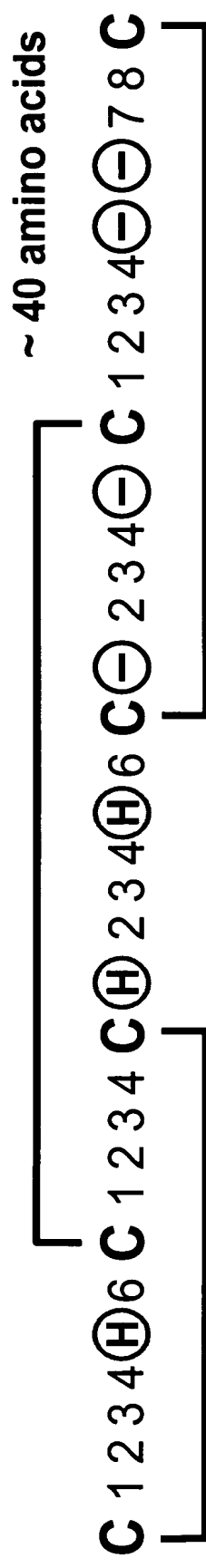
C.1234F6C12G4....CI23456.CDG34DC1D3SDE78....C

FIGURE 3

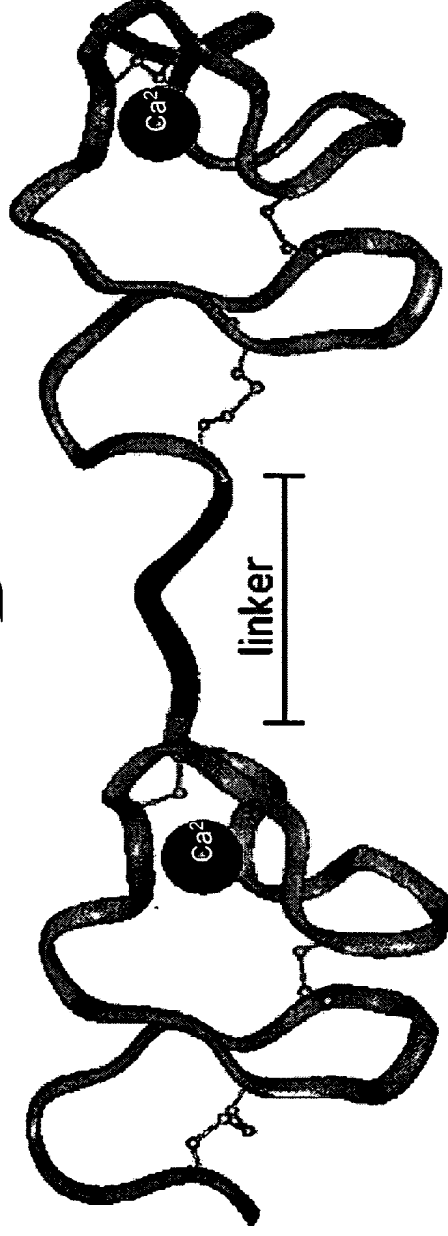
# A-domains

---

A



B



# Figure 4

## Ligands recognized by LDL-receptor family

<i>proteases</i>	<i>proteins involved in</i>	<i>miscellaneous</i>
factor IXa	<i>lipoprotein metabolism</i>	albumin
pro-uPA	apoB100	transthyretin
t-PA	apoE	$\beta$ -Amyloid precursor protein
plasminogen	apoJ (clusterin)	RAP
MMP-9	apoH ( $\beta_2$ -glycoprotein I)	complement C3
	Lp(a)	lactoferrin
<i>inhibitors</i>	hepatic lipase	thyroglobulin
$\alpha_2$ -macroglobulin	lipoprotein lipase	thrombospondin
PAI-1	IDL	saposin precursor
TFPI	VLDL	reelin
pancreatic trypsin inhibitor	$\beta$ -VLDL	insulin
		parathyroid hormone (PTH)
<i>complexes</i>	<i>non-human</i>	aprotinin
protease/	pseudomonas exotoxin A	$\alpha$ -amylase
$\alpha_1$ -antitrypsin	circumsporozoite protein	C1q
protein C inhibitor	trichosanthin	$\alpha_1$ -microglobulin
protease nexin-1	ricin A	$\beta_2$ -microglobulin
antithrombin	saporin	odorant-binding protein
C1-inhibitor		epidermal growth factor
thrombin/heparin cofactor II	<i>antibiotics</i>	prolactin
cathepsin G/ $\alpha_1$ -antichymotrypsin	gentamicin	lysozyme
	polymyxin B	connective tissue growth factor (CTGF)
<i>vitamin-carrier complexes</i>	<i>viruses</i>	cytochrome c
vitamin D-bp, vitamin D	HRV2 (Rhino)	seminal vesicle secretory protein II
retinol-bp, vitamin A	HCV (Flavi)	clara cell secretory protein (CCSP)
transcobalamin, vitamin B12	BVDV (Flavi)	cubulin
		factor VIII

Figure 5

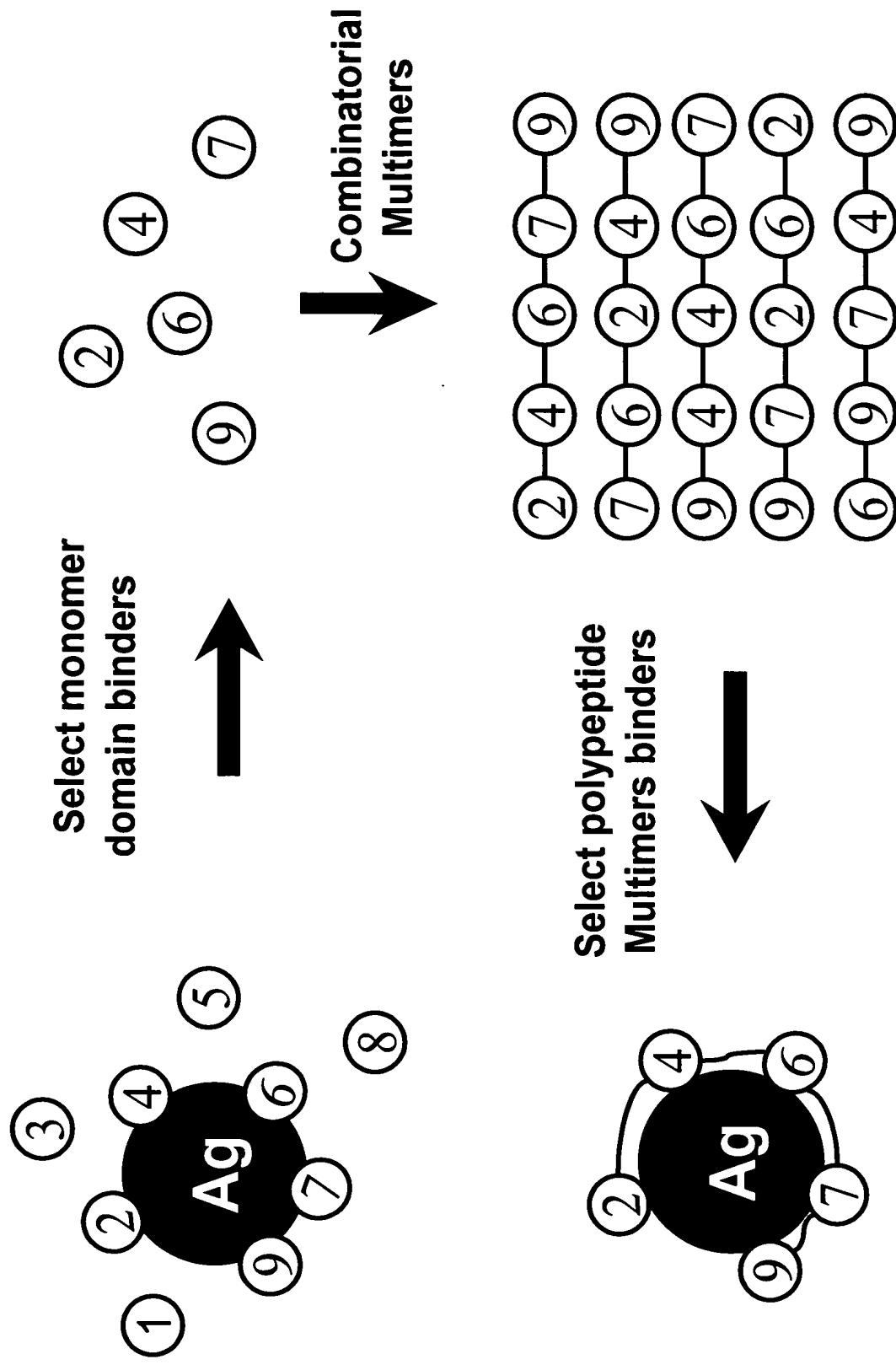


Figure 6

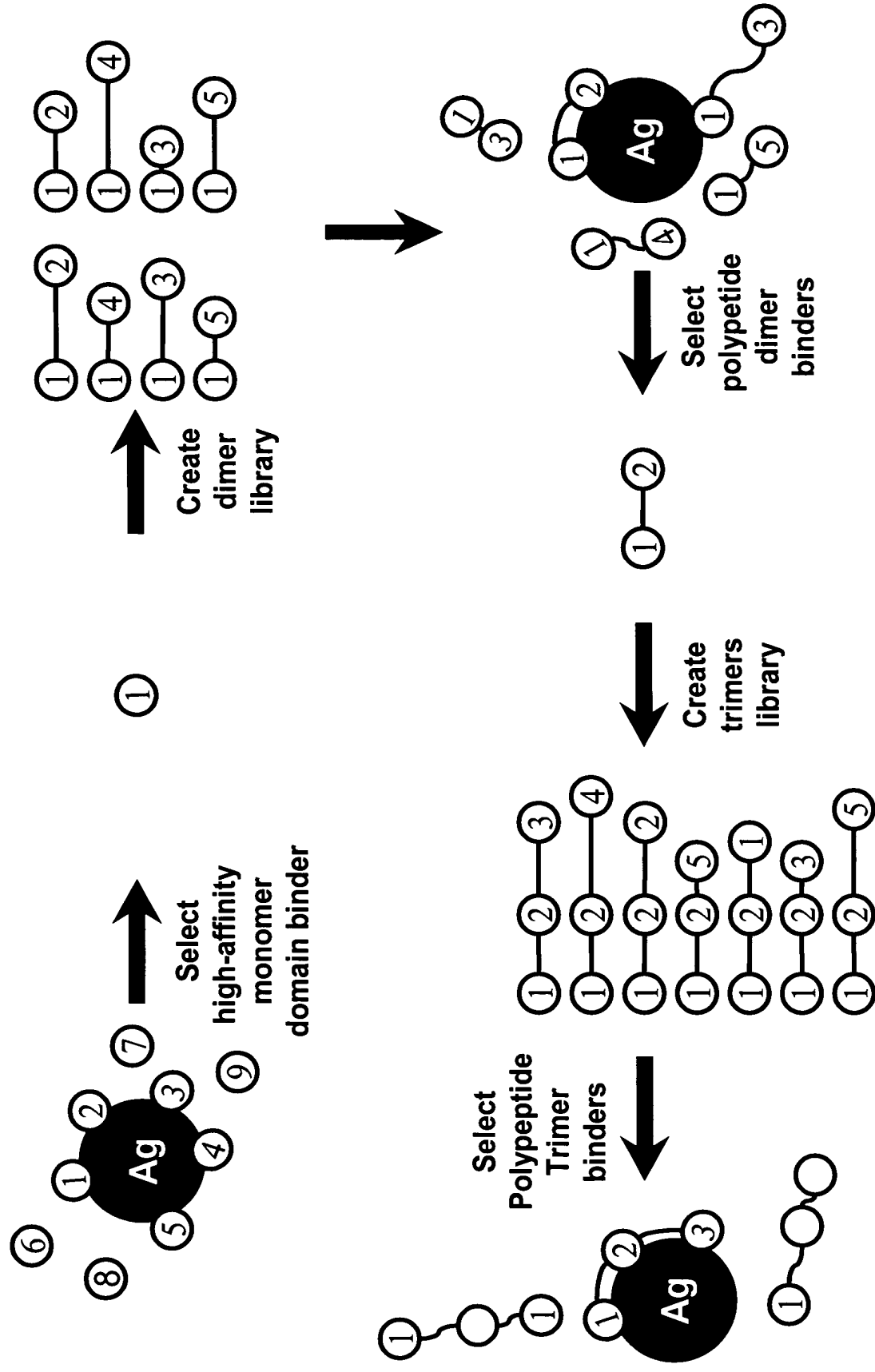


Figure 7

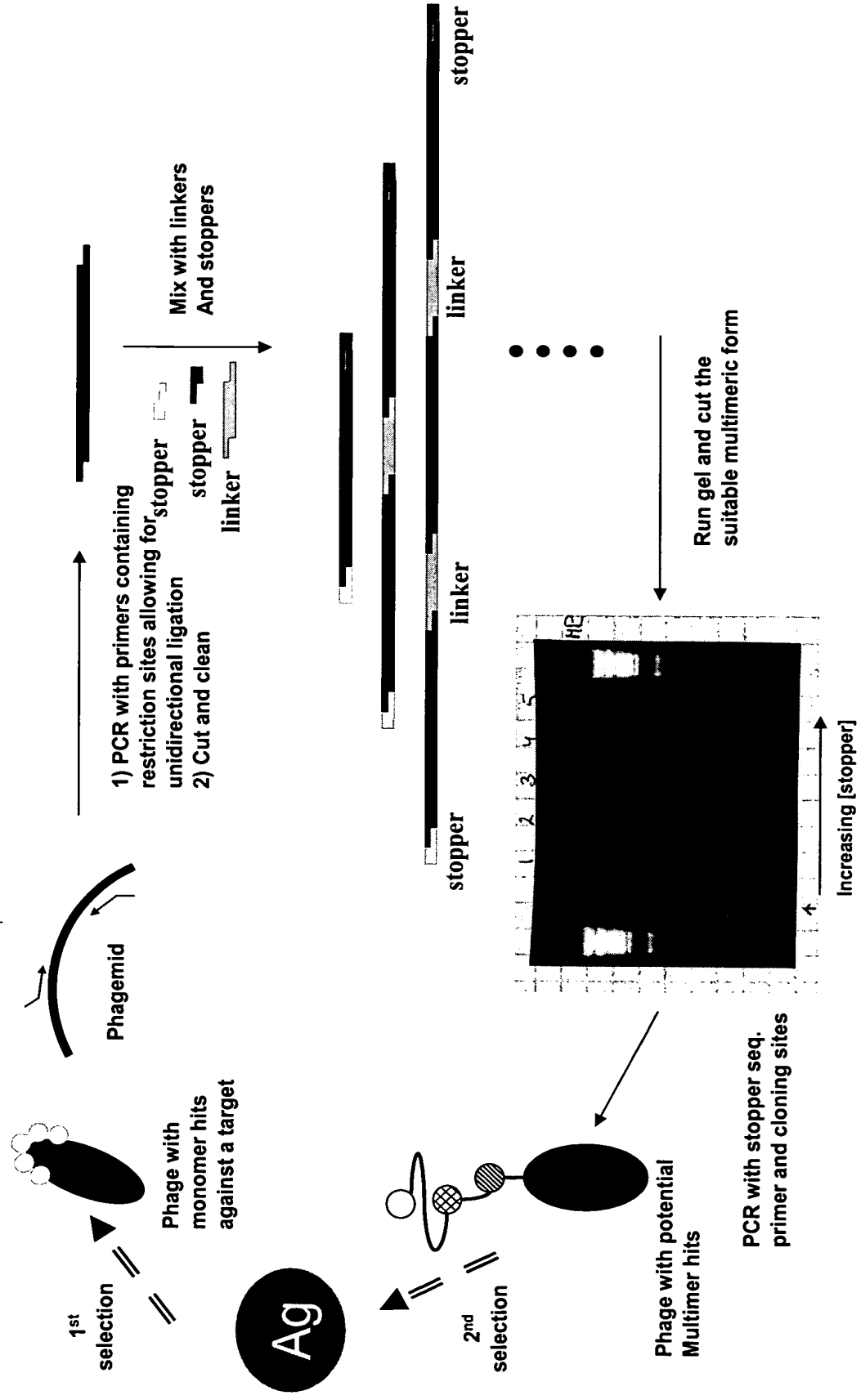






FIG. 9A

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
A	0.0	<u>7.1</u>	12.3	3.2	1.9	1.9	7.1	0.0	15.8	1.5	0.0	1.5	0.0	1.0	3.7	7.3	9.4
C	100.0	0.0	0.6	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	1.5	99.5	0.0	0.0	0.0	0.0
D	0.0	5.2	4.5	19.5	2.6	0.0	0.0	0.0	8.3	<u>10.5</u>	2.3	0.8	0.0	0.0	3.7	1.6	4.7
E	0.0	4.5	9.7	2.6	37.0	0.0	3.9	0.0	3.8	0.0	0.8	9.8	0.0	0.0	1.6	7.3	7.3
F	0.0	0.6	0.0	3.9	1.9	76.0	0.6	0.0	0.8	0.0	0.0	0.8	0.0	0.5	1.6	2.1	2.6
G	0.0	13.0	3.2	16.2	1.9	0.0	0.0	0.0	12.8	0.8	72.2	2.3	0.0	0.0	3.1	<u>5.2</u>	4.2
H	0.0	1.9	1.3	<u>5.2</u>	3.9	1.9	3.9	0.0	3.0	0.8	4.5	9.0	0.0	0.0	4.7	3.1	5.8
I	0.0	0.0	1.3	0.0	0.0	3.9	0.6	0.0	0.0	0.0	0.0	2.3	0.0	63.9	0.0	<u>5.2</u>	3.7
K	0.0	3.9	3.9	1.9	1.9	0.6	<u>7.8</u>	0.0	11.3	0.0	3.0	<u>9.0</u>	0.0	2.1	2.1	<u>9.9</u>	3.7
L	0.0	8.4	4.5	0.0	1.3	3.9	3.9	0.0	1.5	0.0	1.5	4.5	0.0	<u>11.0</u>	<u>5.2</u>	12.0	3.1
M	0.0	0.6	0.6	0.0	1.3	0.6	1.9	0.0	0.0	0.0	0.0	0.8	0.0	0.0	<u>0.5</u>	3.1	1.6
N	0.0	1.9	0.6	13.6	1.3	0.0	1.9	0.0	<u>5.3</u>	51.9	<u>5.3</u>	3.8	0.0	0.0	<u>5.2</u>	4.2	2.6
P	0.0	10.4	33.8	1.3	0.0	0.0	9.7	0.0	4.5	0.0	0.0	0.0	0.0	0.0	45.5	7.3	2.1
Q	0.0	10.4	2.6	1.9	30.5	0.6	21.4	0.0	5.3	0.8	2.3	9.8	0.0	0.0	2.6	5.8	4.7
R	0.0	7.1	3.2	3.2	1.3	0.6	18.2	0.0	<u>7.5</u>	0.8	4.5	32.3	0.0	0.0	1.0	<u>9.4</u>	11.5
S	0.0	18.8	11.7	16.2	3.9	0.6	9.7	0.0	15.0	25.6	3.0	3.0	0.0	0.0	14.7	<u>10.5</u>	20.4
T	0.0	<u>5.2</u>	2.6	<u>5.8</u>	3.2	1.3	<u>7.8</u>	0.0	2.3	<u>6.0</u>	0.8	<u>6.0</u>	0.0	1.6	2.6	0.5	<u>5.8</u>
V	0.0	0.6	1.9	0.6	0.0	0.6	1.3	0.0	2.3	0.8	0.0	3.0	0.0	<u>17.3</u>	0.5	3.1	2.6
W	0.0	0.0	0.6	1.9	0.0	1.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	2.6
Y	0.0	0.0	0.6	2.6	<u>5.8</u>	5.2	0.0	0.0	0.8	0.8	0.0	0.0	0.5	2.6	1.0	2.1	1.6
	100.0	85.7	67.5	76.6	73.4	81.2	81.8	100.0	81.2	94.0	77.4	75.9	99.5	92.1	70.7	80.1	60.2
1	9	4	6	3	2	2	7	1	8	4	2	6	1	3	4	10	6
100.0	73.4	67.5	65.6	67.5	76.0	66.2	66.2	100.0	68.4	77.4	72.2	60.9	99.5	63.9	60.2	60.2	59.2
1	7	4	4	4	2	1	5	1	6	2	1	4	1	1	2	7	6

FIG. 9B

18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
1.6	2.6	0.0	0.0	1.0	2.5	<u>5.6</u>	0.0	0.0	<u>6.9</u>	0.0	4.6	4.6	0.0	0.0	16.0	3.8	0.0
0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
1.0	0.0	0.0	81.2	1.5	28.4	22.3	86.3	0.0	3.8	89.3	1.5	0.0	100.0	0.0	<u>6.9</u>	21.4	0.0
1.0	1.6	0.0	0.0	2.0	15.7	<u>4.6</u>	3.6	0.0	9.9	0.0	2.3	6.9	0.0	100.0	<u>16.8</u>	0.8	0.0
<u>7.9</u>	0.5	0.0	0.0	0.5	4.6	3.0	0.0	0.0	0.0	0.0	0.8	0.0	0.0	0.0	1.5	0.8	0.0
1.0	0.0	0.0	0.0	66.0	0.5	0.0	0.0	0.0	30.5	1.5	48.9	1.5	0.0	0.0	0.8	22.9	0.0
0.0	2.6	0.0	0.0	3.6	4.1	1.5	3.6	0.0	0.8	0.8	2.3	0.0	0.0	0.0	2.3	6.1	0.0
0.0	4.7	0.0	0.0	0.0	4.6	2.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	3.1	0.8	0.0
<u>6.8</u>	<u>12.6</u>	0.0	0.0	1.0	2.5	<u>5.1</u>	0.0	0.0	6.1	0.0	3.8	0.0	0.0	0.0	12.2	0.8	0.0
<u>14.7</u>	15.2	0.0	0.0	1.5	2.0	3.0	0.0	0.0	<u>6.9</u>	0.0	1.5	0.8	0.0	0.0	9.9	0.8	0.0
0.5	1.0	0.0	0.0	1.5	1.0	0.0	0.0	0.0	1.5	0.0	3.1	0.8	0.0	0.0	1.5	0.8	0.0
2.1	0.0	0.0	18.8	3.6	2.0	21.3	4.1	0.0	0.0	4.6	14.5	0.0	0.0	0.0	1.5	33.6	0.0
0.0	0.5	0.0	0.0	0.0	0.0	10.7	0.0	0.0	9.9	0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.0
<u>5.8</u>	<u>7.3</u>	0.0	0.0	4.1	10.7	4.6	1.5	0.0	<u>5.3</u>	0.8	3.1	0.0	0.0	0.0	6.1	0.8	0.0
<u>3.7</u>	24.1	0.0	0.0	5.6	2.5	6.1	0.0	0.0	3.8	0.0	2.3	3.1	0.0	0.0	<u>10.7</u>	1.5	0.0
1.0	0.0	0.0	0.0	3.0	2.0	2.0	0.5	0.0	7.6	1.5	4.6	80.9	0.0	0.0	0.8	4.6	0.0
0.5	2.6	0.0	0.0	2.5	1.5	2.0	0.5	0.0	0.8	0.8	0.0	1.5	0.0	0.0	2.3	0.0	0.0
1.0	21.5	0.0	0.0	0.5	10.2	3.6	0.0	0.0	4.6	0.0	0.0	0.0	0.0	0.0	<u>6.1</u>	0.0	0.0
46.6	2.6	0.0	0.0	0.5	2.0	1.5	0.0	0.0	0.0	0.0	3.1	0.0	0.0	0.0	0.8	0.0	0.0
4.7	0.5	0.0	0.0	1.5	3.0	1.0	0.0	0.0	0.0	0.8	3.8	0.0	0.0	0.0	0.8	0.0	0.0
81.7	80.6	100.0	100.0	71.6	65.0	71.1	86.3	100.0	83.2	89.3	63.4	87.8	100.0	100.0	84.7	84.0	100.0
5	5	1	2	2	4	6	1	1	8	1	2	2	1	1	8	4	1
61.3	60.7	100.0	81.2	66.0	65.0	60.4	86.3	100.0	64.1	89.3	63.4	80.9	100.0	100.0	61.1	77.9	100.0
2	3	1	1	1	4	4	1	1	5	1	2	1	1	1	5	3	1

Figure 10

	a	b c	de	f	ghi	jk	lm	nop	q
IDD_HUMAN	C.....	NPGQFACRSGTIQ.....	CIPLPWQ.CDGWATCEDE.....	SDEAN.....	C				
LRP3_HUMAN	C.....	QADEFRCDNGK.....	CLPGPWQ.CNTVDECGDG.....	SDEGN.....	C				
LRP3_HUMAN	C.....	PGGTFFPCSGARSTR.....	CLPVERR.CDGLQDCGDG.....	SDEAG.....	C				
LRP3_HUMAN	C.....	LPWEQPCGSSSDSDGGS LGDQGC	CFSEPQR.CDGWWHCASG.....	RDEQG.....	C				
LRP3_HUMAN	C.....	PPDQYPCEGGSGL.....	CYTPADR.CNNQKSCPDG.....	ADEKN.....	C				
LRP3_HUMAN	C.....	QPGTFHCGTNL.....	CIFETWR.CDQEDCQDG.....	SDEHG.....	C				
LRP5_HUMAN	C.....	SPDQFACATGEID.....	CIPGAWR.CDGFPECDDQ.....	SDEEG.....	C				
LRP5_HUMAN	C.....	SAAQFPCARGQ.....	CVDLRLR.CDGEADCQDR.....	SDEVD.....	C				
LRP5_HUMAN	C.....	LPNQFRCASGQ.....	CVLIKQQ.CDSFPDCIDG.....	SDELM.....	C				
LRP6_HUMAN	C.....	SPQOFTCFTGEID.....	CIPVAWR.CDGFTECEDH.....	SDELN.....	C				
LRP6_HUMAN	C.....	SESQFQCASGQ.....	CIDGALR.CNGDANCQDK.....	SDEKN.....	C				
LRP6_HUMAN	C.....	LIDQFRCANGQ.....	CIGKHKK.CDHNVDSCDK.....	SDELD.....	C				
ST7_HUMAN	C.....	ACDQFRCNGK.....	CIPPAWK.CNNMDECGDS.....	SDEEI.....	C				
ST7_HUMAN	C.....	AYNQFQCLSRFTKVT.....	CLPESLK.CDGNIDCLDL.....	GDEID.....	C				
ST7_HUMAN	C.....	LPWEIPCGGNWG.....	CYTEQQR.CDGYWHCPNG.....	RDETN.....	C				
ST7_HUMAN	C.....	QKEEFPCSRNGV.....	CYPRSDR.CNYQNHCPNG.....	SDEKN.....	C				
ST7_HUMAN	C.....	QPGNFHCKNNR.....	CVFESWV.CDSQDDCGDG.....	SDEEN.....	C				
CORI_HUMAN	C.....	GRGENFLCASGI.....	CIPGKLQ.CNGYNDCCDDW.....	SDEAH.....	C				
CORI_HUMAN	C.....	SENLFHCHTGK.....	CLNYSLV.CDGYDDCGDL.....	SDEQN.....	C				
CORI_HUMAN	C.....	NPTTEHRCGDGR.....	CIAMEWV.CDGDHDCVDK.....	SDEVN.....	C				
CORI_HUMAN	C.....	HSQGLVECRNGQ.....	CIPSTFQ.CDGEDCKDG.....	SDEEN.....	C				
CORI_HUMAN	C.....	SPSHFKCRSGQ.....	CVLASRR.CDQADCCDD.....	SDEEN.....	C				
CORI_HUMAN	C.....	KERDLWECPSNKQ.....	CLKHTVI.CDGFPCPDY.....	MDEKN.....	C				
CORI_HUMAN	C.....	QDDELECANHA.....	CVSRDLW.CDGEADCSDS.....	SDEWD.....	C				
TMS2_HUMAN	C.....	SNSGIECDSSGT.....	CINPSNW.CDGVSHCPGG.....	EDENR.....	C				
TMS3_HUMAN	C.....	SGKYRCRSSFK.....	CIELIAR.CDGVSDCKDG.....	EDEYR.....	C				
MAT_HUMAN	C.....	PGQFTCRTGR.....	CIRKELR.CDGWADCTDH.....	SDELN.....	C				
MAT_HUMAN	C.....	DAGHQFTCKNKF.....	CKPLFWV.CDSVNDCGDN.....	SDEQG.....	C				
MAT_HUMAN	C.....	PAQTFRCNSNGK.....	CLSKSQQ.CNGKDDCGDG.....	SDEAS.....	C				
MAT_HUMAN	C.....	TKHTYRCLNGL.....	CLSKGNPEC DKEDCSDG.....	SDEKD.....	C				
ENTK_HUMAN	C.....	LPGSSPCTDALT.....	CIKADLF.CDGEVNC PDG.....	SDEDNKM.....	C				
ENTK_HUMAN	C.....	KADHFQCKNGE.....	CVPLVNL.CDGLHLCEDG.....	SDEAD.....	C				
HAI1_HUMAN	C.....	OPTQFRCNSNGC.....	CIDSFLE.CDDTPNCPDA.....	SDEAA.....	C				
CFAI_HUMAN	C.....	YTQKADSPMDDFFQCVNGK.....	YISQMKACDGINDCGDQ.....	SDEL.....	C				
CFAI_HUMAN	C.....	QGKG FHCKSGV.....	CIPSQYQ.CNGEVDCITG.....	EDEVG.....	C				
CO6_HUMAN	C.....	KNKFRCDSGR.....	CIARKLE.CNGENDCGDN.....	SDERD.....	C				
CO7_HUMAN	C.....	GERFRCFSGQ.....	CISKSLV.CNGSDSCDEDS.....	ADEDR.....	C				
CO8A_HUMAN	C.....	GQDFQCKETGR.....	CLKRHLV.CNGDQDCLDG.....	SDEDD.....	C				
CO8B_HUMAN	C.....	EGFVCAQTGR.....	CVNRRLL.CNGDNDCGDQ.....	SDEAN.....	C				
CO9_HUMAN	C.....	GNDFOCSTGR.....	CIKMRLR.CNGDNDCGDF.....	SDEDD.....	C				
PERL_HUMAN	C.....	TEAEFACHSYNE.....	CVALEYR.CDRRDCRDM.....	SDELN.....	C				
PERL_HUMAN	C.....	GPQEAACRNGH.....	CIPRDYL.CDQEDCEDG.....	SDELD.....	C				
PERL_HUMAN	C.....	EPNEFFPCGNH.....	CALKLWR.CDGFDCEDR.....	TDEAN.....	C				
PERL_HUMAN	C.....	GPTQFRCVSTNM.....	CIPASFH.CDEESDCPDR.....	SDEFG.....	C				
SORL_HUMAN	C.....	LRNQYRCNSGN.....	CINSIWW.CDFDNDCGDM.....	SDERN.....	C				
SORL_HUMAN	C.....	DLDTQFRCQESGT.....	CIPLSYK.CDLEDDCGDN.....	SDESH.....	C				
SORL_HUMAN	C.....	RSDEYNCSSEM.....	CIRSSWV.CDGDNDCRDW.....	SDEAN.....	C				
SORL_HUMAN	C.....	EASNFQCRNGH.....	CIPQRWA.CDGDTCQDG.....	SDEDPVN.....	C				
SORL_HUMAN	C.....	NGFRCPNGT.....	CIPSSKH.CDGLRDCSDG.....	SDEQH.....	C				
SORL_HUMAN	C.....	THFMDFVCKNRQQ.....	CLFHSMV.CDGIIQCRDG.....	SDEDAAFAG.....	C				
SORL_HUMAN	C.....	DEFGFQCQNGV.....	CISLIWK.CDGMDDCGDY.....	SDEAN.....	C				
SORL_HUMAN	C.....	SRYFQFRCENGH.....	CIPNRWK.CDRENDCGDW.....	SDEKD.....	C				
SORL_HUMAN	C.....	LPNYYRCSSGT.....	CVMDTWV.CDGYRDCADG.....	SDEEA.....	C				
SORL_HUMAN	C.....	DRFEFECHQPKT.....	CIPNWKR.CDGHQDCQDG.....	RDEAN.....	C				
SORL_HUMAN	C.....	MSREFQCEGGEA.....	CIVLSER.CDGFLLCSDE.....	SDEKA.....	C				
APOER2_HUM	C.....	EKDQFQCRNER.....	CIPSVWR.CDEDDDCLDH.....	SDEDD.....	C				
APOER2_HUM	C.....	ASDFTCDNGH.....	CIHERWK.CDGECECPDG.....	SDESEAT.....	C				
APOER2_HUM	C.....	PAEKLSCGPTSHK.....	CVPASWR.CDGEKDCGEG.....	ADEAG.....	C				
APOER2_HUM	C.....	APHEFQCNGRS.....	CLAAVFW.CDGDGDCGDG.....	SDEAG.....	C				
APOER2_HUM	C.....	GPREFRCGGDGGGA.....	CIPERWV.CDRQFDCEDR.....	SDEAAEL.....	C				
APOER2_HUM	C.....	ATVSQFACRSGE.....	CVHLGWR.CDGRDCKDK.....	SDEAD.....	C				
APOER2_HUM	C.....	RGDEFQCGDGT.....	CVLAIKH.CNQEQDCPDG.....	SDEAG.....	C				
LDLR_HUMAN	C.....	ERNEFQCGDGK.....	CISYKWW.CDGSACQDG.....	SDESQET.....	C				
LDLR_HUMAN	C.....	KSGDFSCGGRVNR.....	CIPQFWR.CDQVDCDNG.....	SDEQG.....	C				
LDLR_HUMAN	C.....	SQDEFRC HDGK.....	CISRQFV.CDSRDCCLDG.....	SDEAS.....	C				
LDLR_HUMAN	C.....	GPASFQCNSSST.....	CIPQLWA.CDNDPDCEDG.....	SDEWQR.....	C				
LDLR_HUMAN	C.....	SAFEFHCLSGE.....	CIHSSWR.CDGGPDCKDK.....	SDEEN.....	C				
LDLR_HUMAN	C.....	RPDEFQCS DGN.....	CIHGSRQ.CDREYDCKDM.....	SDEVG.....	C				
LDLR_HUMAN	C.....	BGPKNFKCHSGE.....	CITLDKV.CNMARDCRDW.....	SDEPIKE.....	C				

LDVR_HUMAN	C.....	EPSQFQCTNGR.....	CITLLWK	CDGDEDCVDG.....	SDEKN.....	C
LDVR_HUMAN	C.....	AESDFVCNNGQ.....	CVPSRWK	CDGDPDCEDG.....	SDESPEQ.....	C
LDVR_HUMAN	C.....	RIHEISCGAHSTQ.....	CIPVSWR	CDGENDCDSDG.....	EDEEN.....	C
LDVR_HUMAN	C.....	SPDEFTCSSGR.....	CISRNFV	CNGQDDCSDG.....	SDELD.....	C
LDVR_HUMAN	C.....	GAHEFQCSTSS.....	CIPISWV	CDDADDCSDQ.....	SDESLEQ.....	C
LDVR_HUMAN	C.....	PASEIQCGSGE.....	CIHKKWR	CDGDPDCKDG.....	SDEVN.....	C
LDVR_HUMAN	C.....	RPDQFECEDGS.....	CIHGSRQ	CNGIRDCVDG.....	SDEVN.....	C
LDVR_HUMAN	C.....	LGPQKFKCRSGE.....	CIDISKV	CNQEQDCRDW.....	SDEPLKE.....	C
LRP1_HUMAN	C.....	SPKQFACRDQIT.....	CISKGWR	CDGERDCPDG.....	SDEAPEI.....	C
LRP1_HUMAN	C.....	QPNEHNCGLTEL.....	CVPM SRL	CNGVQDCMDG.....	SDEGPH.....	C
LRP1_HUMAN	C.....	QPGEFACANSR.....	CIQERWK	CDGDNDCLDN.....	SDEAPAL.....	C
LRP1_HUMAN	C.....	PSDRFKCENNR.....	CIPNRWL	CDGDNDCGNS.....	EDESNAT.....	C
LRP1_HUMAN	C.....	PPNQFSCASGR.....	CIPISWT	CDLDDDCGDR.....	SDESAS.....	C
LRP1_HUMAN	C.....	FPLTQFTCNNGR.....	CININWR	CDNDNDCGDN.....	SDEAG.....	C
LRP1_HUMAN	C.....	SSTQFKCNSGR.....	CIPHEWT	CDGDNDCGDY.....	SDETHAN.....	C
LRP1_HUMAN	C.....	HTDEFQCRLDGL.....	CIPLRWR	CDGDTDCMDS.....	SDEKS.....	C
LRP1_HUMAN	C.....	DPSVKFGCKDSAR.....	CISKAWV	CDGDNDCEDN.....	SDEEN.....	C
LRP1_HUMAN	C.....	RPPSHPCANNTSV.....	CLPPDKL	CDGNDDCGDG.....	SDEGEL.....	C
LRP1_HUMAN	C.....	RAQDEFECANGE.....	CINFSLT	CDGVPHCKDK.....	SDEKPSY.....	C
LRP1_HUMAN	C.....	KKTFRQCSNGR.....	CVSNMLW	CNGADDCGDG.....	SDEIP.....	C
LRP1_HUMAN	C.....	GVGEFRCRDGT.....	CIGNSSR	CNQFVDCEDA.....	SDEM N.....	C
LRP1_HUMAN	CSSYFRLGVKGVLFQPCERTSL.....		CYAPSWV	CDGANDCGDY.....	SDERD.....	C
LRP1_HUMAN	C.....	PLNYFACPSGR.....	CIPMSWT	CDKEDDCHEG.....	EDETH.....	C
LRP1_HUMAN	C.....	SEAQFECQNRH.....	CISKQWL	CDGSDDCGDG.....	SDEAAH.....	C
LRP1_HUMAN	C.....	GPSSFSCPGTHV.....	CVPERWL	CDGDKDCADG.....	ADESIAAG.....	C
LRP1_HUMAN	C.....	DDREFMCONRQ.....	CIPKHV	CDHDRDCADG.....	SDESPE.....	C
LRP1_HUMAN	C.....	GPSEFRCANR.....	CLSSRQWE	CDGENDCHDQ.....	SDEAPKNPH.....	C
LRP1_HUMAN	C.....	NASSQFLCSSGR.....	CVAEALL	CNGQDDCGDS.....	SDE RG.....	C
LRP1_HUMAN	C.....	TASQFVCKNDK.....	CIPFWWK	CDTEDDCGDH.....	SDEPPD.....	C
LRP1_HUMAN	C.....	RPQGFQCSGTI.....	CTNPAFI	CDGDNDCQDN.....	SDEAN.....	C
LRP1_HUMAN	C.....	LPSQFKCTNTNR.....	CIPGIFR	CNGQDNCGDG.....	EDERD.....	C
LRP1_HUMAN	C.....	APNQFQCSITKR.....	CIPRVVW	CDRDND CVDG.....	SDEPAN.....	C
LRP1_HUMAN	C.....	GVDEFRCKDSGR.....	CIPARWK	CDGEDDCGDG.....	SDEPKEE.....	C
LRP1_HUMAN	C.....	EPYQFRCKNNR.....	CVPGRWQ	CDYDND CGDN.....	SDEES.....	C
LRP1_HUMAN	C.....	SESEFSCANR.....	CIAGRWK	CDGDHDCADG.....	SDEKD.....	C
LRP1_HUMAN	C.....	DMDQFQCKSGH.....	CIPLRWR	CDADADCM DG.....	SDEEA.....	C
LRP1_HUMAN	C.....	PLDEFQCNNTL.....	CKPLAWK	CDGEDDCGDN.....	SDENPEE.....	C
LRP1_HUMAN	C.....	PPNRPFRCKNDRV.....	CLWIGRQ	CDGTDNCGDG.....	TDEED.....	C
LRP1_HUMAN	C.....	KDKKEFLCRNQR.....	CLSSSLR	CNMFDDCGDG.....	SDEED.....	C
LRP2_HUMAN	C.....	DSAHFRCGSGH.....	CIPADWR	CDGTKDCSDD.....	ADEIG.....	C
LRP2_HUMAN	C.....	QQGYFKCQSEGQ.....	CIPSSWV	CDQDQDCDDG.....	SDERQD.....	C
LRP2_HUMAN	C.....	SSHQITCSNGQ.....	CIPSEYR	CDHVRDCPDG.....	ADEND.....	C
LRP2_HUMAN	C.....	EQLTCDNGA.....	CYNTSQK	CDWKVDCRDS.....	SDEIN.....	C
LRP2_HUMAN	C.....	LHNEFSCNGE.....	CIPRAYV	CDHDND CQDG.....	SDEHA.....	C
LRP2_HUMAN	C.....	GGYQFTCPSGR.....	CIYQNWV	CDGEDDC KDN.....	GDEDG.....	C
LRP2_HUMAN	C.....	SPREWSCPESGR.....	CISYKVV	CDGILDCPGR.....	EDENNTSTGKYC.....	C
LRP2_HUMAN	C.....	GLFSFPCKNGR.....	CVPNYYL	CDGVDDCHDN.....	SDEQL.....	C
LRP2_HUMAN	C.....	SSSAFTCGHGE.....	CIPAHWR	CDKRND CVDG.....	SDEHN.....	C
LRP2_HUMAN	C.....	LDTQYTCDNHQ.....	CISKNVV	CDTDND CQDG.....	SDEKN.....	C
LRP2_HUMAN	C.....	QPSQFNCPNHR.....	CIDLSFV	CDGDKDCVDG.....	SDEVG.....	C
LRP2_HUMAN	C.....	TASQFKCASGDK.....	CIGVTNR	CDGVFDCSDN.....	SDEAG.....	C
LRP2_HUMAN	C.....	HSDEFQCEQDGI.....	CIPNFWE	CDGHPDCLYG.....	SDEHNA.....	C
LRP2_HUMAN	C.....	PSSYFHCDNGN.....	CIHRAWL	CDRDND CQDM.....	SDEKD.....	C
LRP2_HUMAN	C.....	PSWQWQCLGHNI.....	CVNLSVV	CDGIFDCPNG.....	TDESPL.....	C
LRP2_HUMAN	C.....	GASSFTCSNGR.....	CISEEWK	CDNDND CQDG.....	SDEMESV.....	C
LRP2_HUMAN	C.....	SPTAFTCANR.....	CVQYSYR	CDYYND CQDG.....	SDEAG.....	C
LRP2_HUMAN	C.....	NATTEFMCNNRR.....	CIPREFI	CNGVDNCHDNNT.....	SDEKN.....	C
LRP2_HUMAN	C.....	QSGYTKCHNSNI.....	CIPRVYL	CDGDND CQDN.....	SDENPTY.....	C
LRP2_HUMAN	C.....	SSSEFQCASGR.....	CIPQHWH	CDQETDCFDA.....	SDEPAS.....	C
LRP2_HUMAN	C.....	LADEFKCDGGR.....	CIPSEWI	CDGDND CQDM.....	SDEDKRHQ.....	C
LRP2_HUMAN	C.....	SDSEFLCVNDRPPDRR.....	CIPQSWV	CDGDVDC TDG.....	YDENQN.....	C
LRP2_HUMAN	C.....	SENEFTCGYGL.....	CIPKIFR	CDRHND CQDY.....	SDE RG.....	C
LRP2_HUMAN	C.....	QQNQFTCQNGR.....	CISKTFV	CDEDND CQDG.....	SDELMHL.....	C
LRP2_HUMAN	C.....	PPHEFKCDNGR.....	CIEMMKL	CNHLDDCLDN.....	SDEKG.....	C
LRP2_HUMAN	C.....	SSTQFLCANNEK.....	CIPIWVK	CDGQKDCSDG.....	SDELAL.....	C
LRP2_HUMAN	C.....	RLGQFQCSQDN.....	CTSPQTL	CNAHQNC PDG.....	SDEDRLL.....	C
LRP2_HUMAN	C.....	DSNEWQCANKR.....	CIPESWQ	CDTFND CEDN.....	SDESSSH.....	C
LRP2_HUMAN	C.....	RPQGFRCANR.....	CIPQAWK	CDVDND CQDH.....	SDEPIEE.....	C
LRP2_HUMAN	C.....	DNFTEFSCKTNYR.....	CIPKWAV	CNGVDD CDRN.....	SDEQG.....	C
LRP2_HUMAN	C.....	HPVGDFRCKNHH.....	CIPLRWQ	CDGQND CQDN.....	SDEEN.....	C
LRP2_HUMAN	C.....	TESEFRVCNQG.....	CIPSRWI	CDHYND CQDN.....	SDERD.....	C
LRP2_HUMAN	C.....	HPEYFQCTSGH.....	CVHSELK	CDGSADCLDA.....	SDEAD.....	C
LRP2_HUMAN	C.....	QATMFECKNHV.....	CIPPYWK	CDGDDDCGDG.....	SDEELHL.....	C
LRP2_HUMAN	C.....	NSPNRFRCDNRR.....	CIYSHEV	CNGVDD CQDG.....	TDETEEH.....	C
LRP2_HUMAN	C.....	TEYEYKCGNGH.....	CIPHNDV	CDDADDCGDW.....	SDELG.....	C
LR1B_HUMAN	C.....	DPGEFLCHDHVT.....	CVSQSWL	CDGDPDCPDD.....	SDES LDT.....	C

LR1B_HUMAN	C.....	PLNHIACLGTNK.....	CVHLSQL.CNGVLDCPDG.....	YDEGVH.....	C
LR1B_HUMAN	C.....	KAGEFRCKNRH.....	CIQARWK.CDGDDDCLDG.....	SDEDSVN.....	C
LR1B_HUMAN	C.....	PDDQFKCQNR.....	CIPKRWL.CDGANDCGSN.....	EDESNQT.....	C
LR1B_HUMAN	C.....	QVDQFSCGNGR.....	CIPRAWL.CDREDDCGDQ.....	TDEMAS.....	C
LR1B_HUMAN	C.....	EPLTQFVCKSGR.....	CISSEKH.CDSDDDCGDG.....	SDEVG.....	C
LR1B_HUMAN	C.....	FDNQFRCSGR.....	CIPGHWL.CDGDNDCGDF.....	SDEAQIN.....	C
LR1B_HUMAN	C.....	NGNEFQCHPDGN.....	CVPDLWR.CDGEKDCEDG.....	SDEKG.....	C
LR1B_HUMAN	C.....	DHKTFCSCWSTGR.....	CINKAWV.CDGDIDCEDQ.....	SDEDD.....	C
LR1B_HUMAN	C.....	GPPKHPCANDTSV.....	CLQPEKL.CNGKKDCPDG.....	SDEGYL.....	C
LR1B_HUMAN	C.....	NAYSEFECNGE.....	CIDYQLT.CDGIPHCCKDK.....	SDEKLLY.....	C
LR1B_HUMAN	C.....	RRGFKPCYNRR.....	CIPHGKL.CDGENDCGDN.....	SDELD.....	C
LR1B_HUMAN	C.....	ATVEFRCADGT.....	CIPRSAR.CNQNICADA.....	SDEKN.....	C
LR1B_HUMAN	C.....	CTHFYKLGVKTTGFIRCNSTSL.....	CVLPTWI.CDGSNDCGDY.....	SDELK.....	C
LR1B_HUMAN	C.....	EENYFSCPSGR.....	CILNTWI.CDGQKDCEDG.....	RDEFH.....	C
LR1B_HUMAN	C.....	SWNQFACSAQK.....	CISKHWI.CDGEDDCGDG.....	LDESISI.....	C
LR1B_HUMAN	C.....	AADMFSCQGSRA.....	CVPRHWL.CDGERDCPDG.....	SDELSTAG.....	C
LR1B_HUMAN	C.....	DENAFMCHNKV.....	CIPKQFV.CDHDDDCGDG.....	SDESPQ.....	C
LR1B_HUMAN	C.....	GTEEFSCADGR.....	CLLNTQWQCDGDFDCPDH.....	SDEAPLNPK.....	C
LR1B_HUMAN	C.....	NSSFFMCKNGR.....	CIPSGGL.CDNKDDCGDG.....	SDEAN.....	C
LR1B_HUMAN	C.....	TASQFRCKTDK.....	CIPFWWK.CDTVDDCGDG.....	SDEPDD.....	C
LR1B_HUMAN	C.....	QPGRFQCGTGL.....	CALPAFI.CDGENDCGDN.....	SDELN.....	C
LR1B_HUMAN	C.....	LSGQFKCTKNQK.....	CIPVNLN.CNGQDDCGDE.....	EDERD.....	C
LR1B_HUMAN	C.....	SPDYFQCKTTKH.....	CISKLWV.CDEDPCADA.....	SDEAN.....	C
LR1B_HUMAN	C.....	GPHEFQCKNNN.....	CIPDHWR.CDSQNDCCSDN.....	SDEEN.....	C
LR1B_HUMAN	C.....	TLKDFLCANGD.....	CVSSRFW.CDGFDFCADG.....	SDERN.....	C
LR1B_HUMAN	C.....	SKDQFRCSNGQ.....	CIPAKWK.CDGHEDECKYG.....	EDEKS.....	C
LR1B_HUMAN	C.....	SSREYICASDG.....	CISASLK.CNGEYDCADG.....	SDEMD.....	C
LR1B_HUMAN	C.....	KEDQFRCKNKAH.....	CIPIRWL.CDGIHDCVDG.....	SDEEN.....	C
LR1B_HUMAN	C.....	RADEFLCNNSL.....	CKLHFVW.CDGEDDCGDN.....	SDEAPDM.....	C
LR1B_HUMAN	C.....	PSTRPHRCRNNRI.....	CLQSEQM.CNGIDECGDN.....	SDEDH.....	C
LR1B_HUMAN	C.....	KKDEFACSNKK.....	CIPMDLQ.CDRLDDCGDG.....	SDEQG.....	C

075851	C.....	AEGEALCQENGH.....	CVPHGWL.CDNQDDCGDG.....	SDEEGE.....	C
075851	C.....	GEGQMTCSSEH.....	CLPLALL.CDRQDDCGDG.....	TDEPSYP.....	C
075851	C.....	PQGLLACADGR.....	CLPPALL.CDGHPDCLDA.....	ADEES.....	C
075851	C.....	VPGEVSCVDGT.....	CLGAIQL.CDGVWDCPDG.....	ADEGPGH.....	C

ENSP00000262089

= 075851

ENSP00000262089	C.....	GPFEFRCSGE.....	CTPRGWR.CDQEEDCADG.....	SDERG.....	C
-----------------	--------	-----------------	-------------------------	------------	---

	C.....	APHHAPCARGPH.....	CVSPEQL.CDGVRQCPDG.....	SDEGPDA.....	C
--	--------	-------------------	-------------------------	--------------	---

075851	C.....	PGLFPCGVAPGL.....	CLTPEQL.CDGIPDCPDG.....	EDELN.....	C
--------	--------	-------------------	-------------------------	------------	---

075851	C.....	PEYTCPNGT.....	CIGFQLV.CDGQPDGCRPGQVGPSPEEQ.....		C
--------	--------	----------------	-----------------------------------	--	---

075851	C.....	EPGVGLRCASGE.....	CVLRGGP.CDGVLDCEDEG.....	SDEEG.....	C
--------	--------	-------------------	--------------------------	------------	---

ENSP00000262089

	C.....	GPGQTPCEVLG.....	CVEQAQV.CDGREDCLDG.....	SDERH.....	C
--	--------	------------------	-------------------------	------------	---

075851	C.....	SPSQLSCSGE.....	CLSAERR.CDLRPDCQDG.....	SDEEG.....	C
--------	--------	-----------------	-------------------------	------------	---

C18ORF1	C.....	KFTCTSGK.....	CLYLGLSLVCNQNDCCGDN.....	SDEEN.....	C
---------	--------	---------------	--------------------------	------------	---

AAH07083/Q9NPF0	C.....	PPTKFQCRTSGL.....	CVPLTWR.CDRDLDCSDG.....	SDEEE.....	C
-----------------	--------	-------------------	-------------------------	------------	---

AAH07083/Q9NPF0	C.....	LAGELRCTLSDD.....	CIPLTWR.CDGHPDCPDG.....	SDELG.....	C
-----------------	--------	-------------------	-------------------------	------------	---

Q9HBX9	C.....	SLGYFPCGNITK.....	CLPQLLH.CNGVDDCGNQ.....	AEDN.....	C
--------	--------	-------------------	-------------------------	-----------	---

Q9BY79/Q96DQ9	C.....	AHDEFRCQDLI.....	CLLPDSV.CDGFANCADG.....	SDETN.....	C
---------------	--------	------------------	-------------------------	------------	---

Q9BY79/Q96DQ9	C.....	GPSELSCQAGG.....	CKGVQWM.CDMWRDCTDG.....	SDDN.....	C
---------------	--------	------------------	-------------------------	-----------	---

BAB55257 =

ENSP00000239367

	C.....	SRYHFFCDDGC.....	CIDITLA.CDGVQCCPDG.....	SDEDF.....	C
--	--------	------------------	-------------------------	------------	---

095518 =	C.....	PGEFLCSVNGL.....	CVPA.....	CDGVKDCPNG.....	LDERN.....	C
----------	--------	------------------	-----------	-----------------	------------	---

ENSP00000255793

ENSP00000255793

	C.....	RATFQCKEDST.....	CISLPKV.CDGQPDCLNG.....	SDEEQ.....	C
--	--------	------------------	-------------------------	------------	---

ENSP00000255793

	C.....	GTFTFQCEDRS.....	CVKKPNPQCDGRPDCTDG.....	SDEEH.....	C
--	--------	------------------	-------------------------	------------	---

	C.....	QKGYFPCGNLTK.....	CLPRAFH.CDGKDDCGNG.....	ADEEN.....	C
--	--------	-------------------	-------------------------	------------	---

Q8WXD0	C.....	STARYHCKNGL.....	CIDKFSI.CDGQNNCQDN.....	SDEES.....	C
--------	--------	------------------	-------------------------	------------	---

Q8NB0	C.....	GPTFFPCASGIH.....	CIIGRFR.CNGFEDCPDG.....	SDEEN.....	C
-------	--------	-------------------	-------------------------	------------	---

Q8NB0	C.....	NIPGNFMCSNGR.....	CIPGAWQ.CDGLPDCFDK.....	SDEKE.....	C
-------	--------	-------------------	-------------------------	------------	---

MEGF7	C.....	ALDQFLCWNGR.....	CIGQRKL.CNGVNDCCGDN.....	SDESPQQN.....	C
-------	--------	------------------	--------------------------	---------------	---

MEGF7	C.....	EEDEFPCQNGY.....	CIRSLWH.CDGDNDCCGDN.....	SDEQ.....	C
-------	--------	------------------	--------------------------	-----------	---

MEGF7	C.....	RSGEFMCDSGL.....	CINAGWR.CDGDADCDQ.....	SDERN.....	C
-------	--------	------------------	------------------------	------------	---

MEGF7	C.....	TAEQFRCHSGR.....	CVRLSWR.CDGEDDCADN.....	SDEEN.....	C
-------	--------	------------------	-------------------------	------------	---

MEGF7	C.....	SPLDFHCDNGK.....	CIRRSWV.CDGDNDCCEDD.....	SDEQD.....	C
-------	--------	------------------	--------------------------	------------	---

MEGF7	C.....	NLEEFQCAAGR.....	CILDIYH.CDGDDDCGDW.....	SDESD.....	C
-------	--------	------------------	-------------------------	------------	---

MEGF7	C.....	SDKEFRCSGDS.....	CIAEHVY.CDGDTCCKDG.....	SDEEN.....	C
-------	--------	------------------	-------------------------	------------	---

MEGF7	C	GRSHFTCAVSALGE <u>C</u> T	CIPAQQWQ	CDGDNDCCGDH	SDEDG	C
CAD61944	C	LQEEFQCLNHR	CVSAVQR	CDGVDACGDG	SDEAG	C
CAD61944	C	PPGHFPCGAAGTSGATA	CYLPADR	CNYQTFCADG	ADERR	C
CAD61944	C	QPGNFRCRDEK	CVYETWV	CDGQPDCCADG	SDEWD	C
ENSG00000181006						
	C	PEITDFLCRDKK	CIASHLL	CDYKPDCSDR	SDEAH	C
ENSP00000320248						
	C	NNRTFKCGNDI	CFRKQNAKCDGTVDCCPDG		SDEEG	C
ENSP00000277547						
	C	PPGHHHCQNKV	CVEPQQQL	CDGEDNCCGDL	SDENPLT	C
ENSP00000320022						
	C	KQGHLCAGDL	CVPPEQL	CDFEEQCAGG	EDEQA	C
ENSP00000313222						
	C	PGNSFSCGNSQ	CVTKVNPECDDQEDCCSDG		SDEAH	C

Figure 11

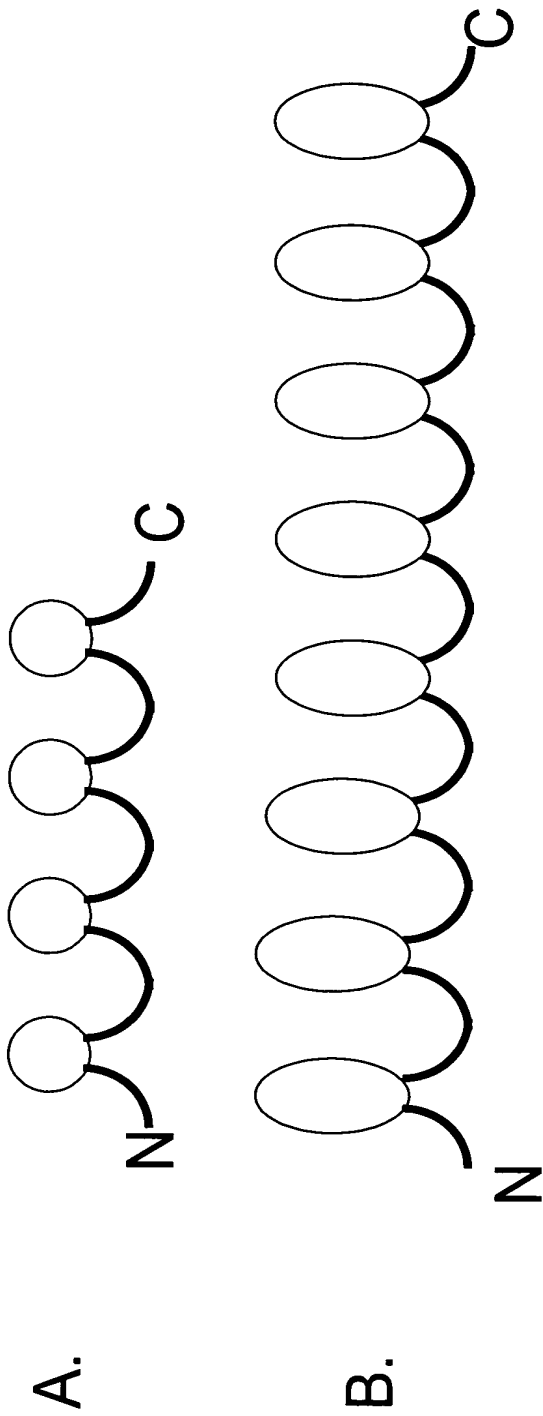
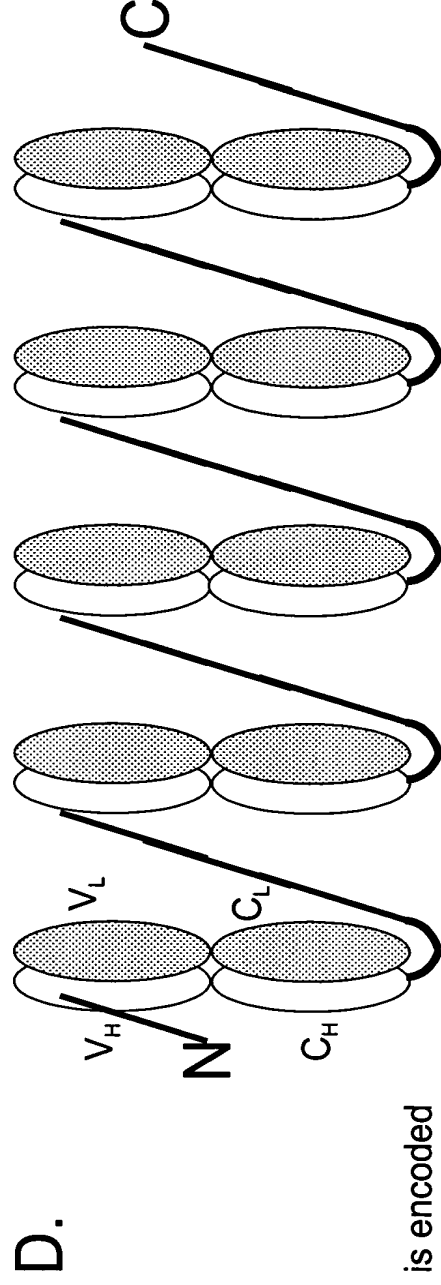
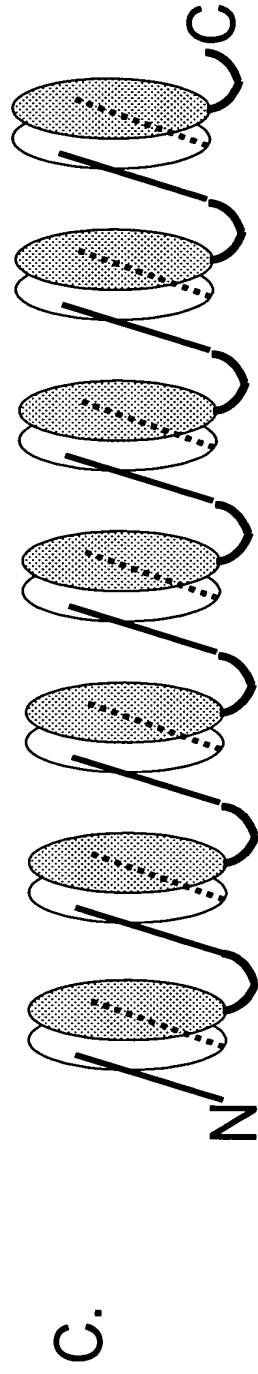


Figure 11



Light chain is encoded  
as a separate protein

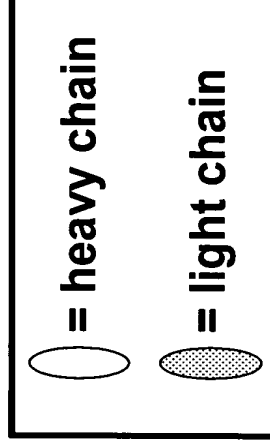
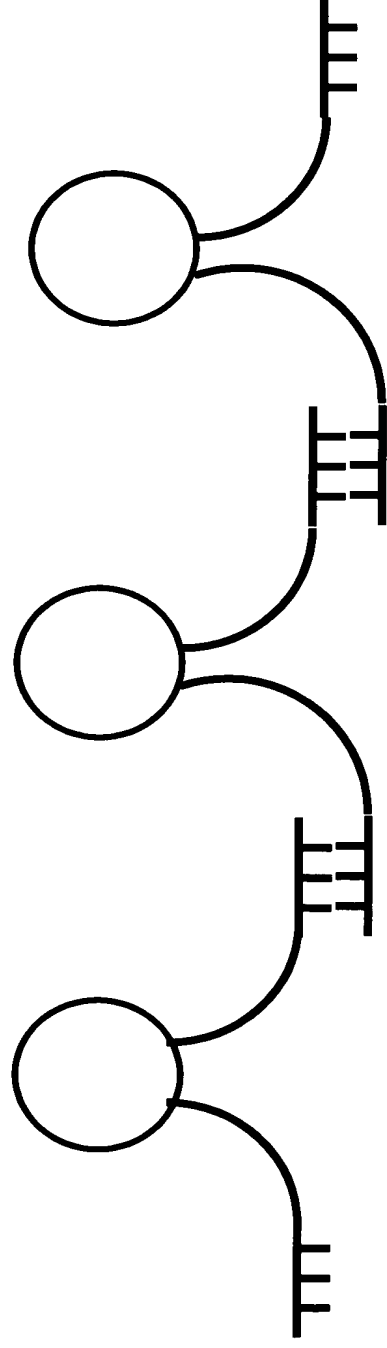




Figure 12

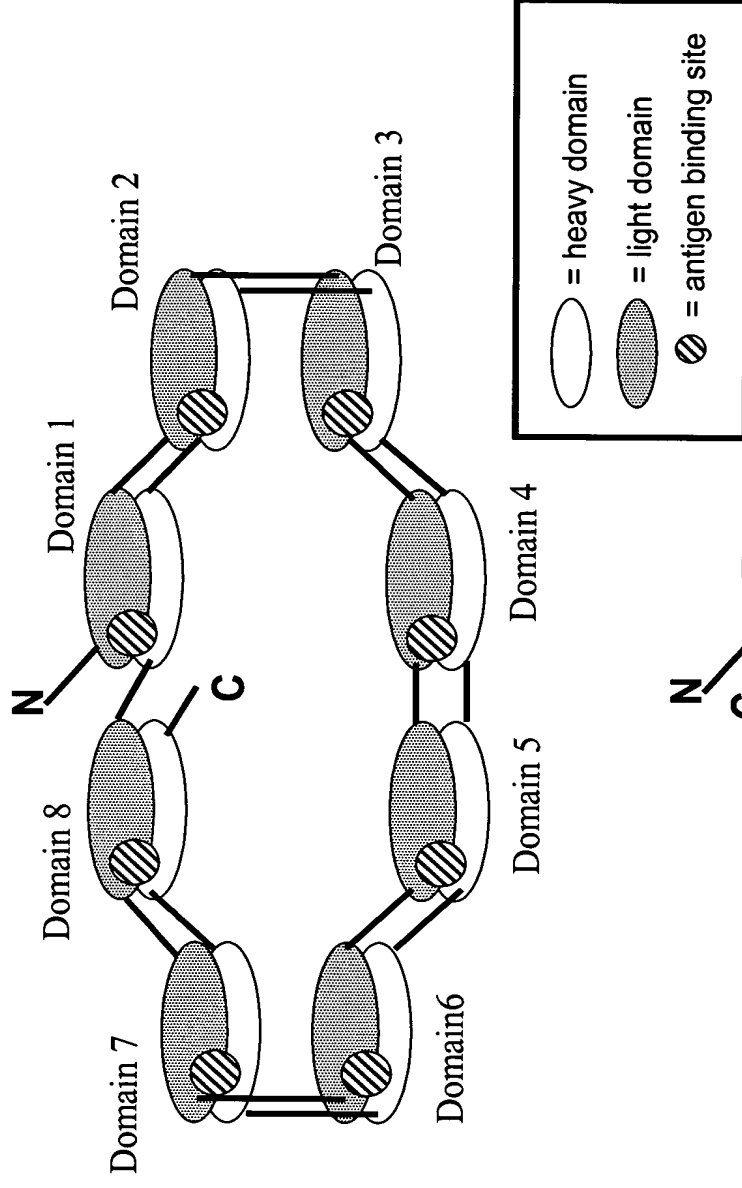


○ = any monomer domain  
▬ = obligate heterodimeric linker

Figure 13

A.

One Chain  
Multimer of  
Fv's



B.

Two Chain  
Multimer of  
Fv's

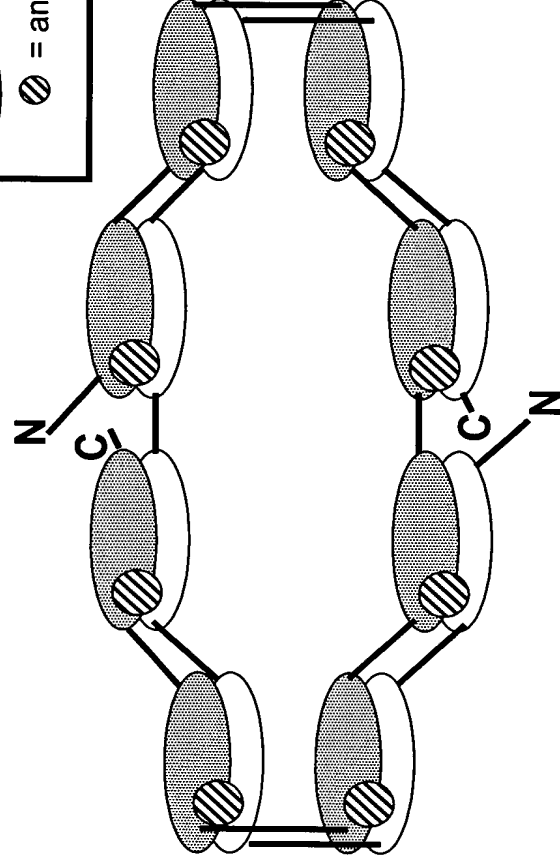


Figure 13C

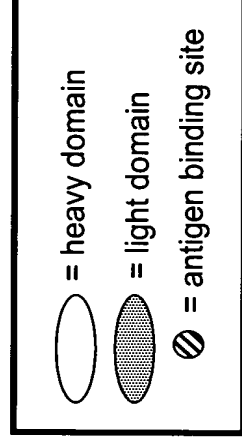
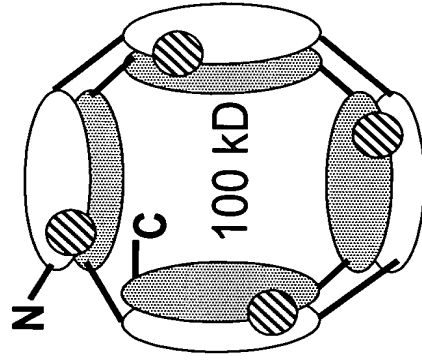


Figure 14

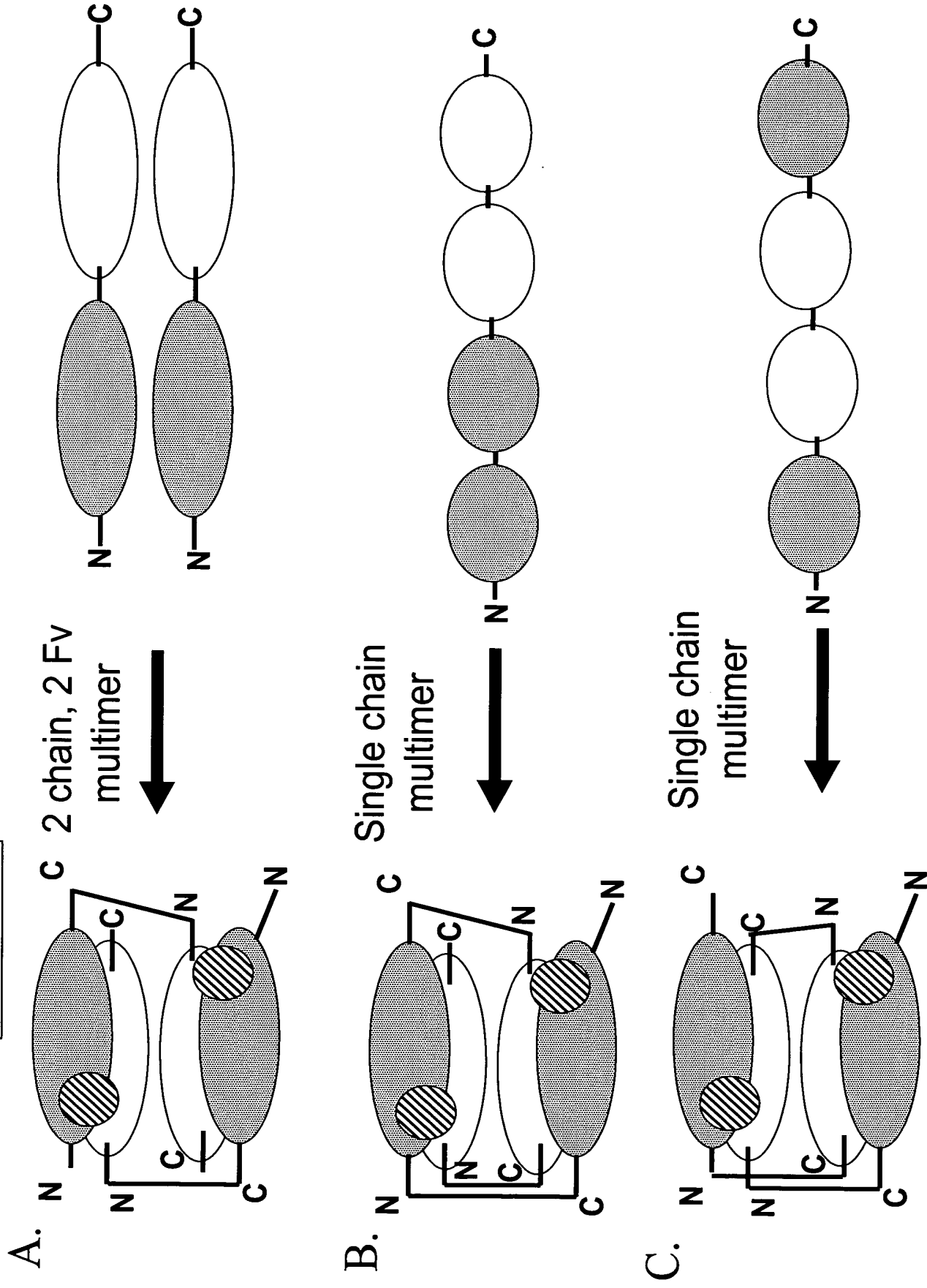
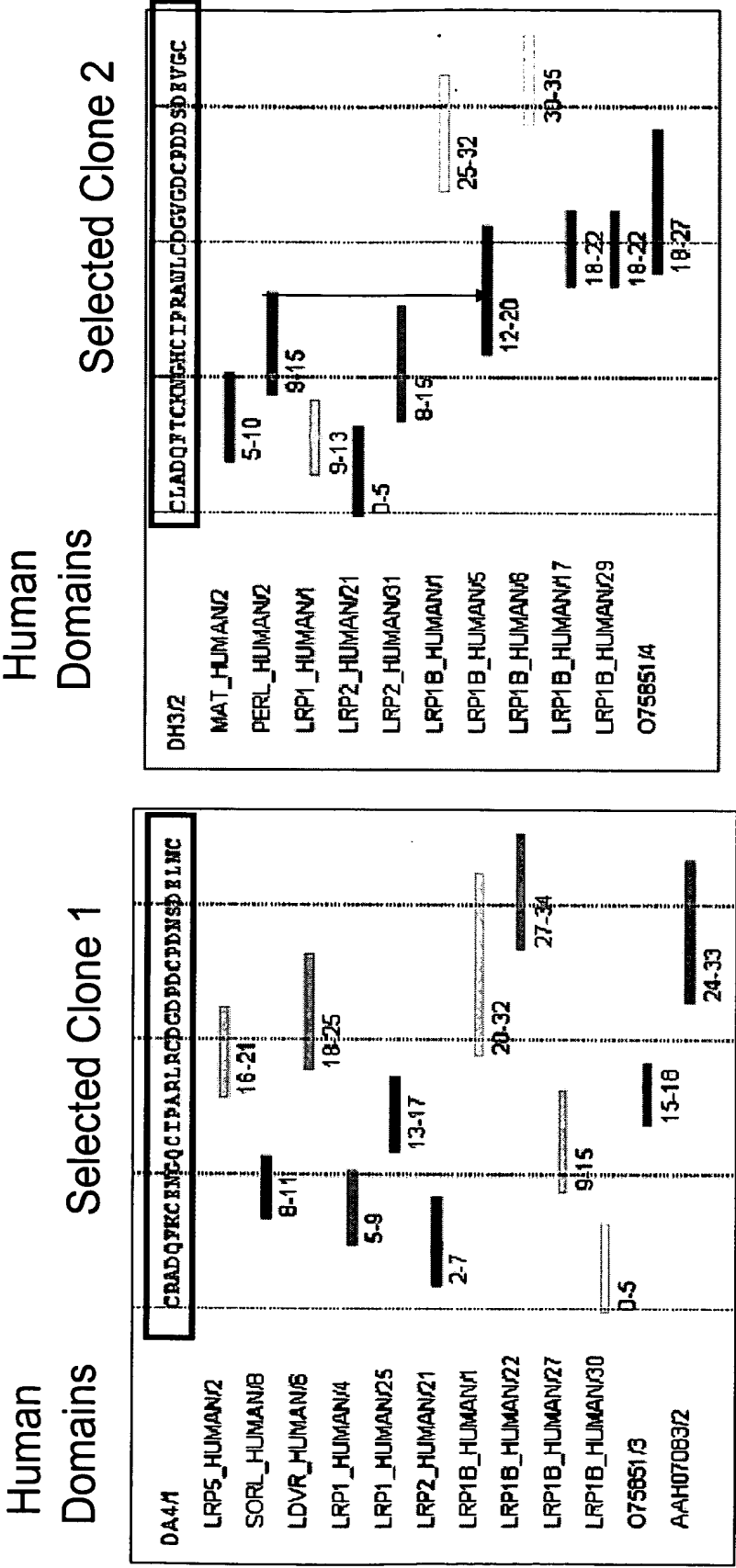


Figure 15



**Figure 16**  
**Cell Killing induced by Maxybodies**

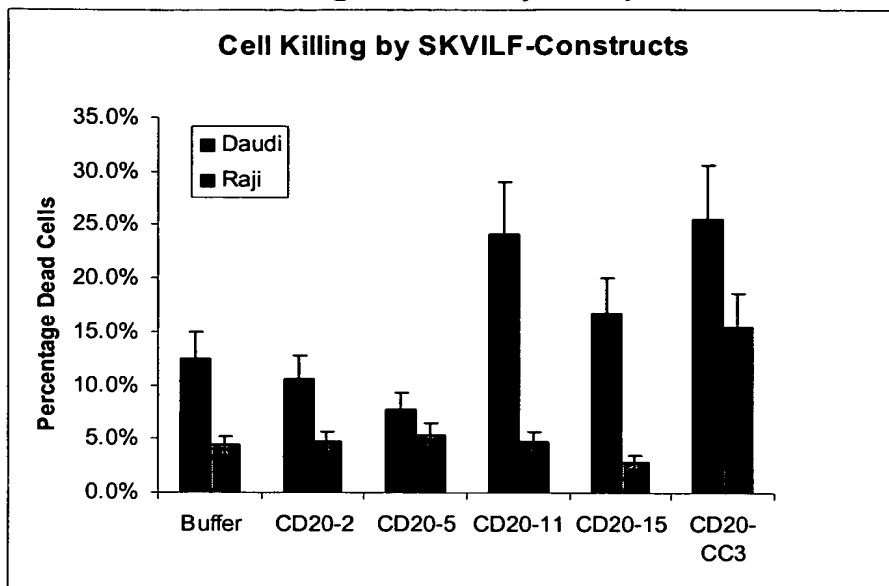


Figure 17: TPO-R Phage Specificity Data

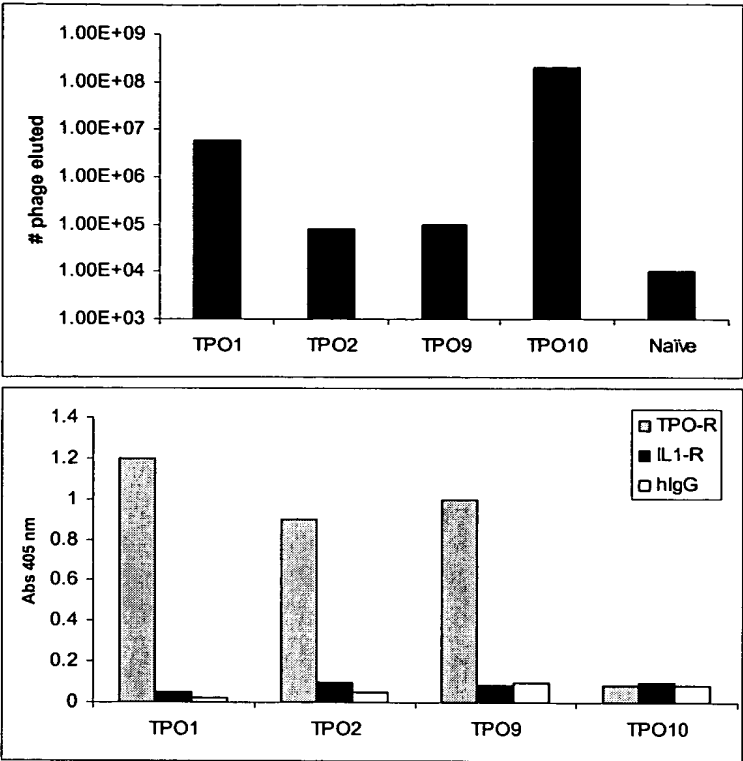
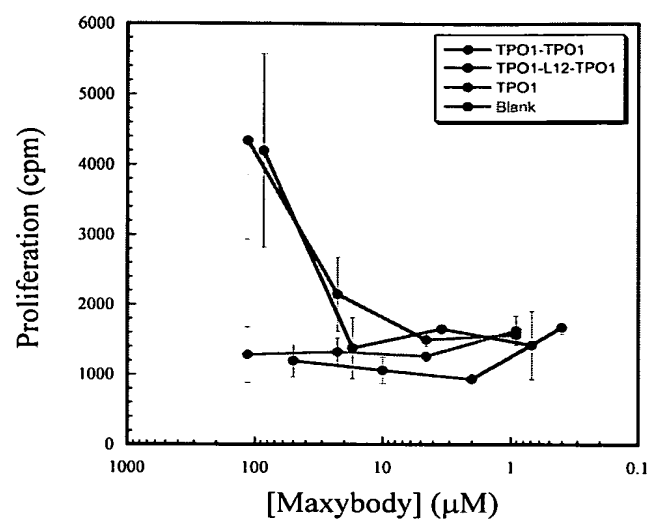
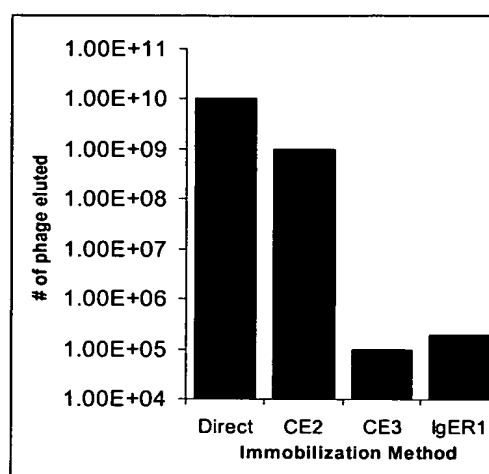


Figure 18: TF1 Proliferation Assay





**Figure 19 : Epitope mapping of IgE-Binding Monomer**



**Figure 20**

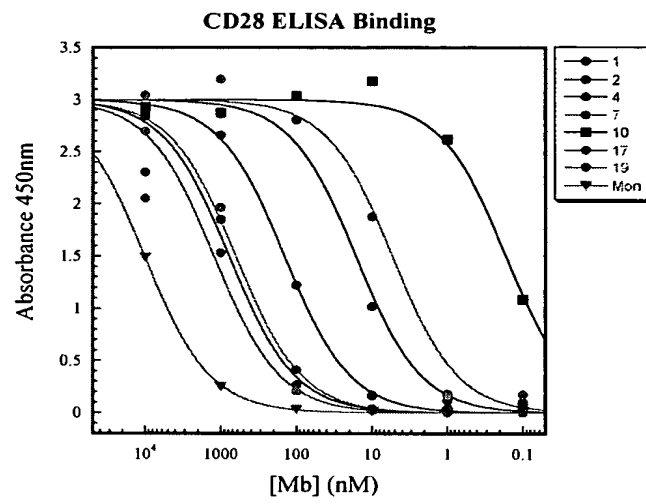


Figure 21

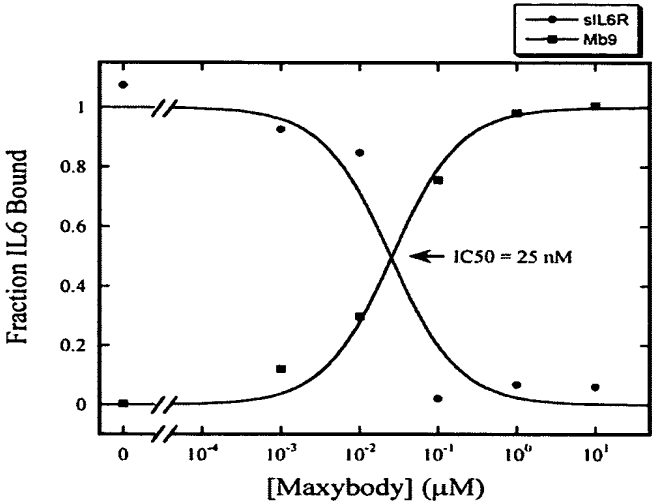


Figure 22

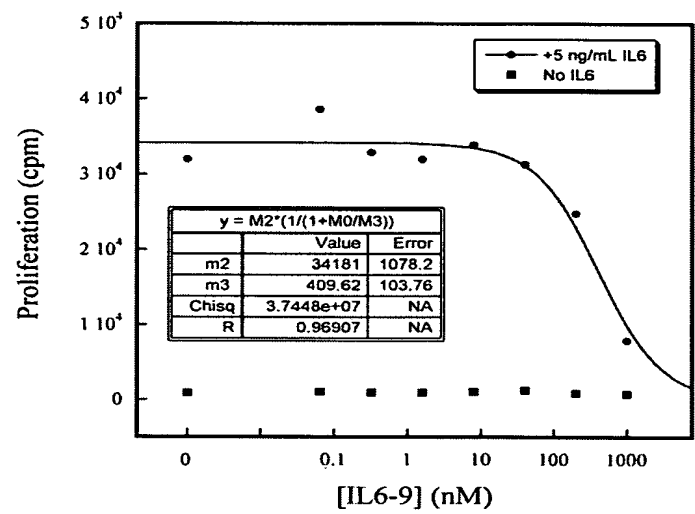
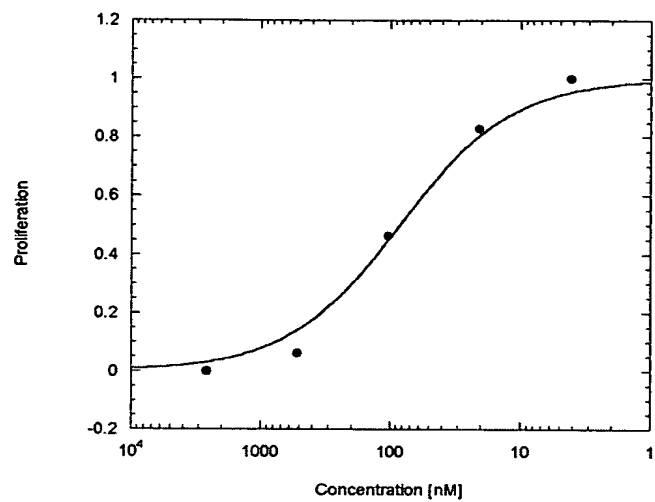


Figure 23



**Figure 24**

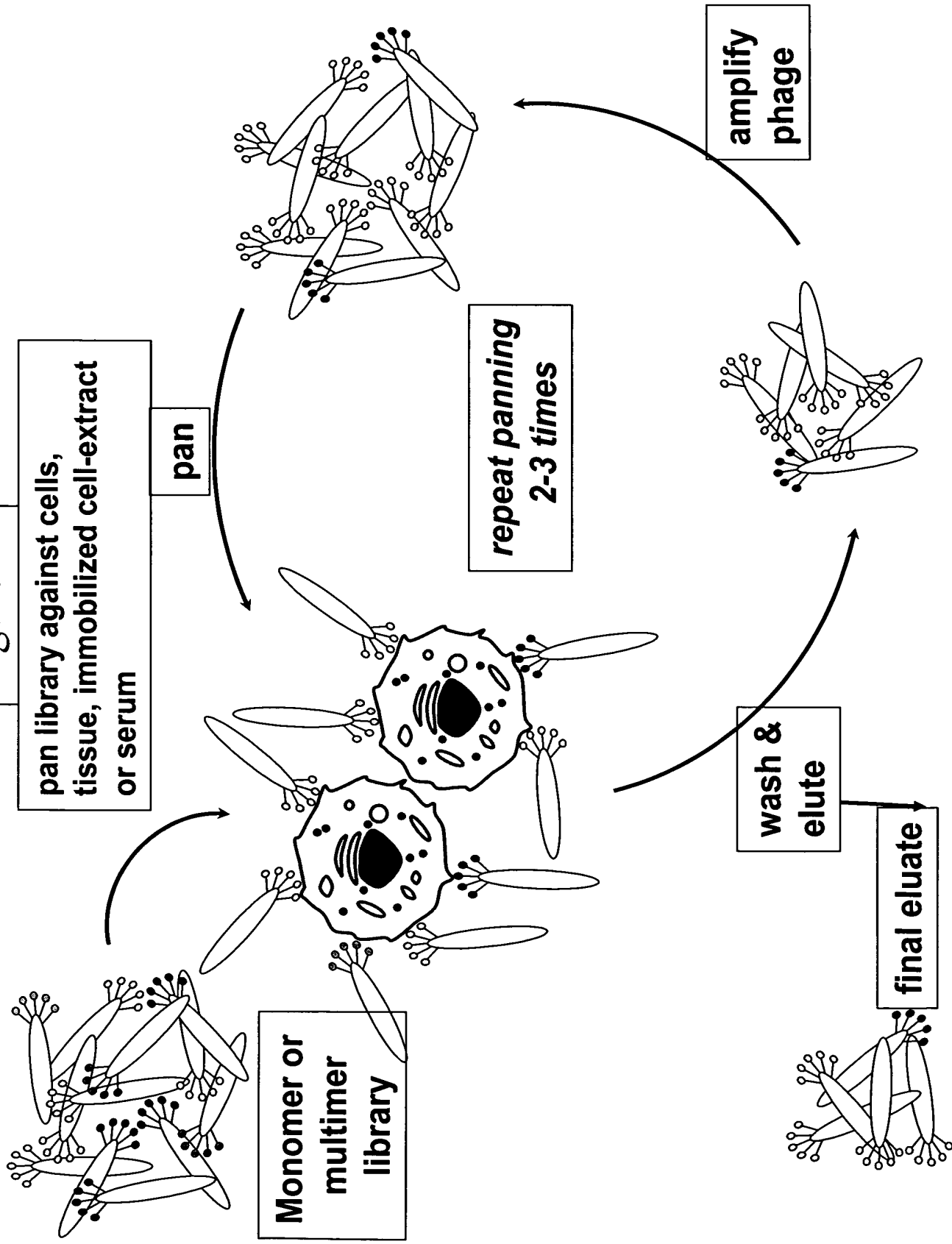


Figure 25

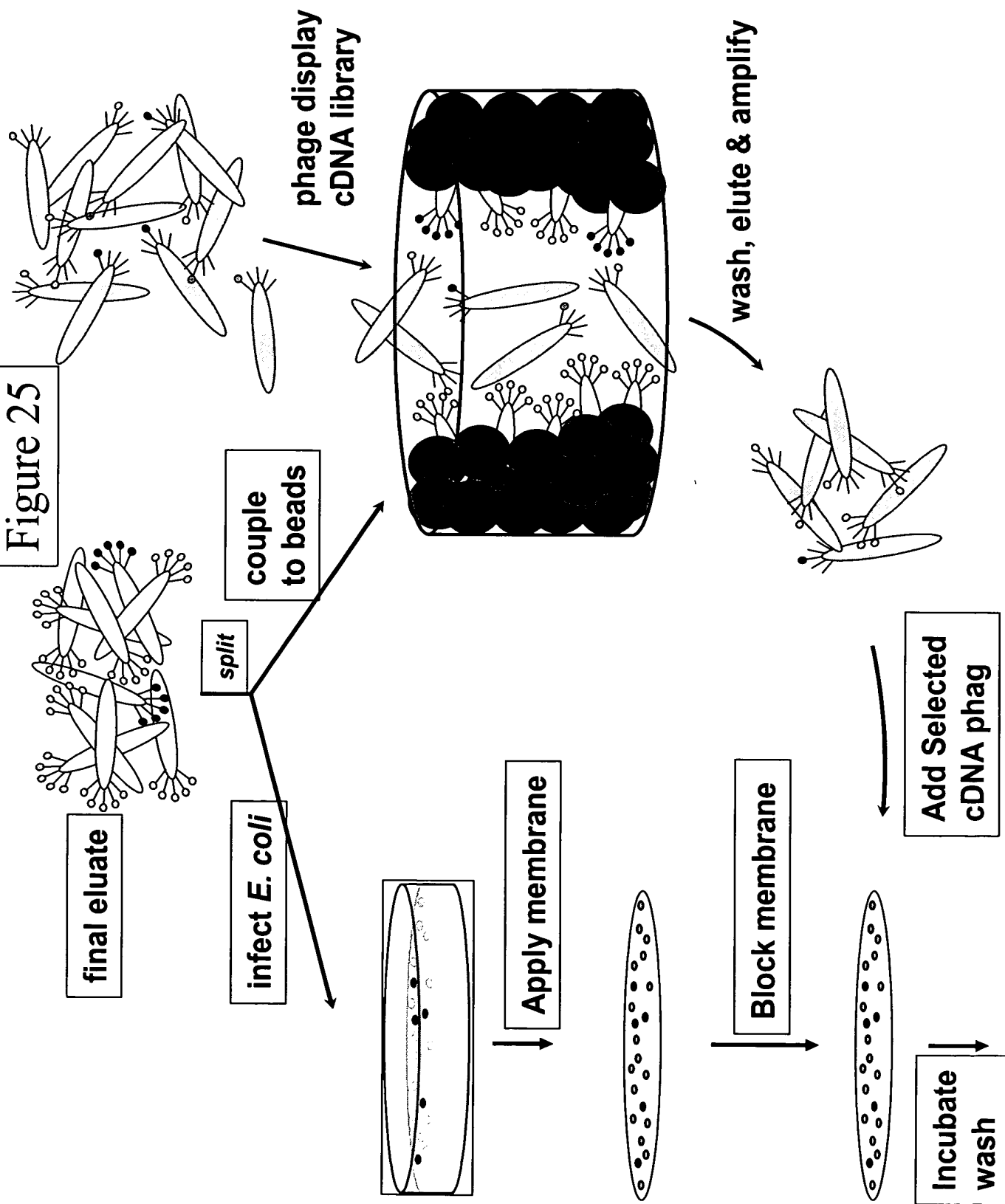
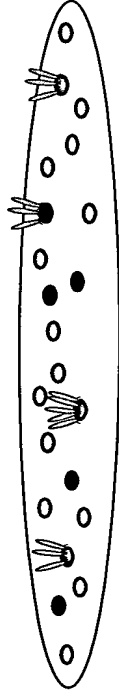
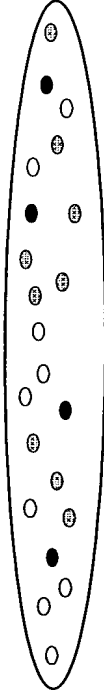


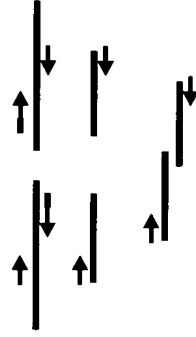
Figure 26



Stain membrane using cDNA phage specific MAb (HRP labeled)  
Add substrate



Cut positive spots out of membrane and add to PCR tube  
PCR amplify cDNA and MB sequences



Sequence PCR fragments



Figure 27

# Format Variations

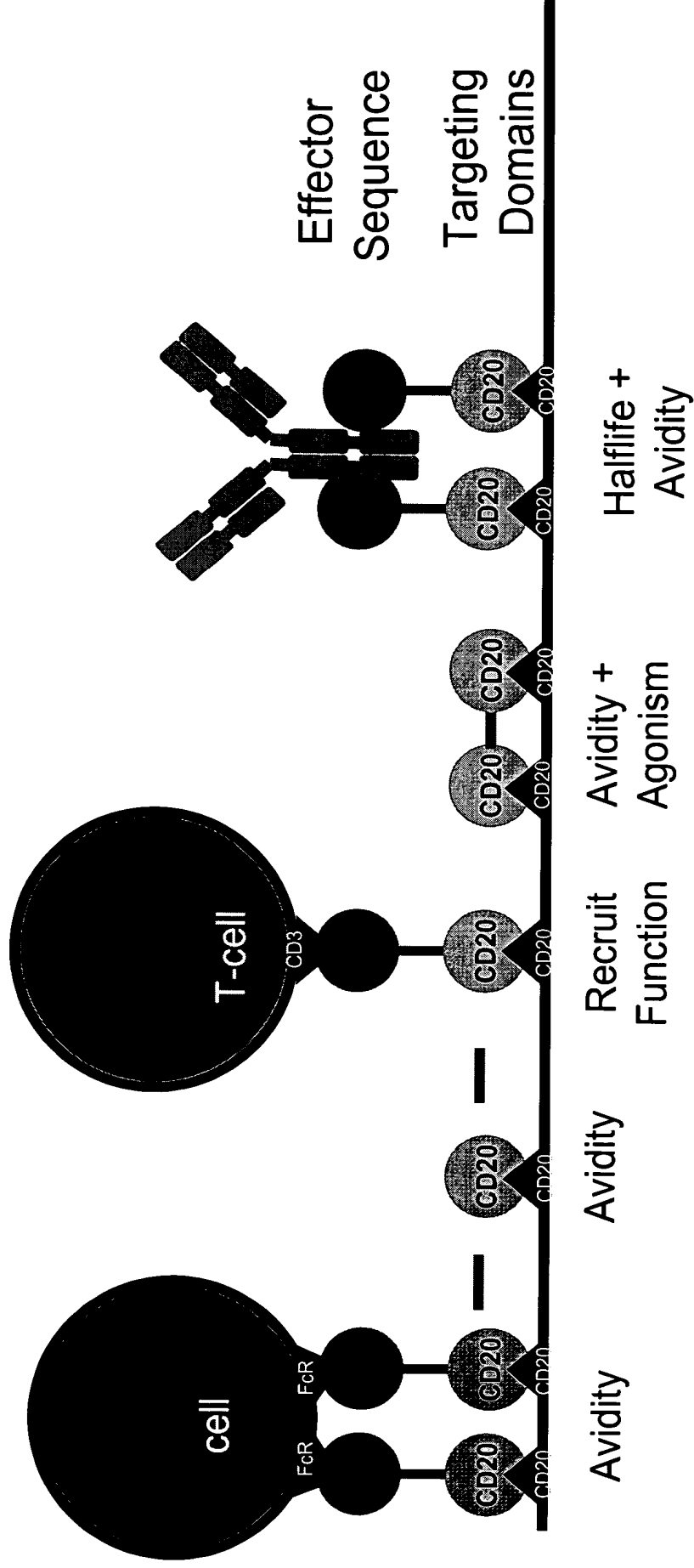
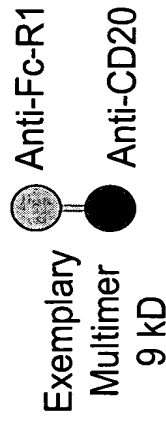


Figure 28

## Multimer Format



Monovalent Binding

Complex Stabilization

